

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 13:48:03 ; Search time 6978.47 Seconds

(without alignments)
11880.962 Million cell updates/secTitle: US-08-153-397A-1
Copyright score: 3962

Sequence: 1 CGGGCCTGAGACTGGGTGA.....AAAAAAACCGGAATT 3962

Scoring table: IDENTITY_NUC

GPop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: *

1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_v1: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_v1: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_oInv: *

ALIGNMENTS

RESULT	1
168738	168738
LOCUS	168738
DEFINITION	Sequence 1 from patent US 5677144.
ACCESSION	3962 bp
VERSION	DNA
KEYWORDS	Linear
SOURCE	PAT 04-FEB-1998
ORGANISM	Unknown.
REFERENCE	Unclassified. (bases 1 to 3962)
AUTHORS	Ulrich,A. and Alves,F.Hildegarde.Elisabeth.
TITLE	Recombinant DNA encoding CCK2, a receptor tyrosine kinase
JOURNAL	Patent: US 5677144-A 14-OCT-1997;
FEATURES	Location/Qualifiers
source	1. 3962 /organism="unknown"
BASE COUNT	735 a 1234 c 1182 g 811 t
ORIGIN	S77556 Ptk-3S-radi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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Query Match	Score	Match Length	DB ID
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Best Local Similarity	Score	3962	DB 6	Length 3962
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Best Local Similarity	Score	3962	DB 6	Length 3962
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Matches	3962:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:	
1	CGGCGCTGAGACTGGGNGACTGGGACCTAAGAGAATCTGAGCTGGAGGGCCCCGAG	60	QY	1081	ACTATGGGATGGNGAACCCACAGCTTCCAGTGCTATGGAGATGGATTGAGT	1140	Db	1081	ACTATGGGATGGNGAACCCACAGCTTCCAGTGCTATGGAGATGGATTGAGT	
Db	CGGCGCTGAGACTGGGNGACTGGGACCTAAGAGAATCTGAGCTGGAGGGCCCCGAG	60	QY	1141	TTGACGGCTGAGGGCCTTCAGGGCTATCAGGTCACITGAACAACTGACACGCGG	1200	Db	1141	TTGACGGCTGAGGGCCTTCAGGGCTATCAGGTCACITGAACAACTGACACGCGG	
61	CTGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	120	QY	121	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	120	Db	121	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	
Db	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	120	QY	121	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	120	Db	121	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	
121	CTGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	120	QY	121	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	120	Db	121	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	
Db	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	120	QY	121	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	120	Db	121	CCGCTCTCGAGGAGCGCCCTCCGACACCCGAGGCCGCGCCGCGCCCTCCGAG	
181	CCCGGGTCTGGACCGCTGGGTCTGGGAGAGGGATGAGGTGCTGAAGGTGGCTAT	240	QY	181	CCCGGGTCTGGACCGCTGGGTCTGGGAGAGGGATGAGGTGCTGAAGGTGGCTAT	240	Db	181	CCCGGGTCTGGACCGCTGGGTCTGGGAGAGGGATGAGGTGCTGAAGGTGGCTAT	
Db	CCCGGGTCTGGACCGCTGGGTCTGGGAGAGGGATGAGGTGCTGAAGGTGGCTAT	240	QY	241	TCACTGAGGGATGGGTTGGACTTGAGGATGCCAGAGATCTGCCCCACCCCTTA	300	QY	241	TCACTGAGGGATGGGTTGGACTTGAGGATGCCAGAGATCTGCCCCACCCCTTA	300
301	GGCCGAGGGATGGGACTATGGGACCGAGGCCCTTCATCTTACTTGCGCTGCT	360	QY	301	GGCCGAGGGATGGGACTATGGGACCGAGGCCCTTCATCTTACTTGCGCTGCT	360	Db	301	GGCCGAGGGATGGGACTATGGGACCGAGGCCCTTCATCTTACTTGCGCTGCT	
Db	GGCCGAGGGATGGGACTATGGGACCGAGGCCCTTCATCTTACTTGCGCTGCT	360	QY	361	TGGTGCCTGAGGGATGCTGAGTGAAGGGGATTTGACCTGCGCAAGTGGCGCTAT	420	QY	361	TGGTGCCTGAGGGATGCTGAGTGAAGGGGATTTGACCTGCGCAAGTGGCGCTAT	420
361	TGGTGCCTGAGGGATGCTGAGTGAAGGGGATTTGACCTGCGCAAGTGGCGCTAT	420	Db	361	TGGTGCCTGAGGGATGCTGAGTGAAGGGGATTTGACCTGCGCAAGTGGCGCTAT	420	Db	361	TGGTGCCTGAGGGATGCTGAGTGAAGGGGATTTGACCTGCGCAAGTGGCGCTAT	
421	CCCTGGGATGCGAGGACCGGACCATCCAGACGACTGAGCATCTCTGCTGCTCAG	480	QY	421	CCCTGGGATGCGAGGACCGGACCATCCAGACGACTGAGCATCTCTGCTGCTCAG	480	Db	421	CCCTGGGATGCGAGGACCGGACCATCCAGACGACTGAGCATCTCTGCTGCTCAG	
Db	CCCTGGGATGCGAGGACCGGACCATCCAGACGACTGAGCATCTCTGCTGCTCAG	480	QY	481	CAGATTCACCTGCGCCGACAGCAGGTGAGGACAGGGATGGGCCTGT	540	QY	481	CAGATTCACCTGCGCCGACAGCAGGTGAGGACAGGGATGGGCCTGT	540
481	CAGATTCACCTGCGCCGACAGCAGGTGAGGACAGGGATGGGCCTGT	540	Db	481	CAGATTCACCTGCGCCGACAGCAGGTGAGGACAGGGATGGGCCTGT	540	Db	481	CAGATTCACCTGCGCCGACAGCAGGTGAGGACAGGGATGGGCCTGT	
541	GGCCGAGGGCTGGGTTCCAAAGGGGAGGACTGCGAGTGTACCTGAGGCTACACAC	600	QY	541	GGCCGAGGGCTGGGTTCCAAAGGGGAGGACTGCGAGTGTACCTGAGGCTACACAC	600	Db	541	GGCCGAGGGCTGGGTTCCAAAGGGGAGGACTGCGAGTGTACCTGAGGCTACACAC	
Db	GGCCGAGGGCTGGGTTCCAAAGGGGAGGACTGCGAGTGTACCTGAGGCTACACAC	600	QY	601	TCCACCTGGCTGCTGGGGACCCGAGGAGGATGGCTGCGCTCTACCCCCAGGT	660	QY	601	TCCACCTGGCTGCTGGGGACCCGAGGAGGATGGCTGCGCTCTACCCCCAGGT	660
601	TCCACCTGGCTGCTGGGGACCCGAGGAGGATGGCTGCGCTCTACCCCCAGGT	660	Db	601	TCCACCTGGCTGCTGGGGACCCGAGGAGGATGGCTGCGCTCTACCCCCAGGT	660	Db	601	TCCACCTGGCTGCTGGGGACCCGAGGAGGATGGCTGCGCTCTACCCCCAGGT	
661	TCTCCCGGAGCTACCGGGTGGTTACCGGGATGGCTGCGCTGAGGGATGGAGG	720	QY	661	TCTCCCGGAGCTACCGGGTGGTTACCGGGATGGCTGCGCTGAGGGATGGAGG	720	Db	661	TCTCCCGGAGCTACCGGGTGGTTACCGGGATGGCTGCGCTGAGGGATGGAGG	
Db	TCTCCCGGAGCTACCGGGTGGTTACCGGGATGGCTGCGCTGAGGGATGGAGG	720	QY	721	ACCGCTGGGGTCAAGGACCTGAGGAGGACTGCGAGTGTACCTGAGGCTGAGG	780	QY	721	ACCGCTGGGGTCAAGGACCTGAGGAGGACTGCGAGTGTACCTGAGGCTGAGG	780
721	ACCGCTGGGGTCAAGGACCTGAGGAGGACTGCGAGTGTACCTGAGGCTGAGG	780	Db	721	ACCGCTGGGGTCAAGGACCTGAGGAGGACTGCGAGTGTACCTGAGGCTGAGG	780	Db	721	ACCGCTGGGGTCAAGGACCTGAGGAGGACTGCGAGTGTACCTGAGGCTGAGG	
781	ACCTGGGCCCCATGGTGGCCGCTCTACCCCCAGCTAACCGGGCTAACCGGGTCA	840	QY	781	ACCTGGGCCCCATGGTGGCCGCTCTACCCCCAGCTAACCGGGCTAACCGGGTCA	840	Db	781	ACCTGGGCCCCATGGTGGCCGCTCTACCCCCAGCTAACCGGGCTAACCGGGTCA	
781	ACCTGGGCCCCATGGTGGCCGCTCTACCCCCAGCTAACCGGGCTAACCGGGTCA	840	QY	841	TGAGTGCTGCTGGGGTAGAGCTTATGGGGATGGCTGGGGTAGAGCTGGAGG	900	QY	841	TGAGTGCTGCTGGGGTAGAGCTTATGGGGATGGCTGGGGTAGAGCTGGAGG	900
841	TGAGTGCTGCTGGGGTAGAGCTTATGGGGATGGCTGGGGTAGAGCTGGAGG	900	Db	841	TGAGTGCTGCTGGGGTAGAGCTTATGGGGATGGCTGGGGTAGAGCTGGAGG	900	Db	841	TGAGTGCTGCTGGGGTAGAGCTTATGGGGATGGCTGGGGTAGAGCTGGAGG	
901	ACACCGGCCCTGGGGCAGCAATGTTATCTGAGGCTGCTACACGACTCCA	960	QY	901	ACACCGGCCCTGGGGCAGCAATGTTATCTGAGGCTGCTACACGACTCCA	960	Db	901	ACACCGGCCCTGGGGCAGCAATGTTATCTGAGGCTGCTACACGACTCCA	
Db	ACACCGGCCCTGGGGCAGCAATGTTATCTGAGGCTGCTACACGACTCCA	960	QY	961	CTCATGAGGGACATACGGTGGGGTAGAGCTTATGGGGATGGCTGGGGTAGAG	1020	QY	961	CTCATGAGGGACATACGGTGGGGTAGAGCTTATGGGGATGGCTGGGGTAGAG	1020
961	CTCATGAGGGACATACGGTGGGGTAGAGCTTATGGGGATGGCTGGGGTAGAG	1020	QY	1021	GTGTGGGGGGCTGGATGACTTGTAGGAGAGTCAGGAGCTGGGGTAGAGCT	1080	QY	1021	GTGTGGGGGGCTGGATGACTTGTAGGAGAGTCAGGAGCTGGGGTAGAGCT	1080
Db	GTGTGGGGGGCTGGATGACTTGTAGGAGAGTCAGGAGCTGGGGTAGAGCT	1080	QY	2101	GGCCAGTGGGGATGGCCCCAGAGTGGATTCCTCGAGTCTCGAGTCTCGCTCAG	2160	QY	2101	GGCCAGTGGGGATGGCCCCAGAGTGGATTCCTCGAGTCTCGAGTCTCGCTCAG	2160

QY	2161	AGAAGCTTGGCGAGGGCCAGTTGGGGGGTGCACCTTGAGGTCCACASCCCTCAAG	2220	Db	
QY	2161	AGAAGCTTGGCGAGGGCCAGTTGGGGGGTGCACCTTGAGGTCCACASCCCTCAAG	2220	Db	3241 CTGATGCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC
QY	2221	ATCTGGTCAGTCGTGATTTCGCCCTTAATGTCGCTAAGGGACACCTTTCGCGTGTAGTG	2280	QY	
QY	2221	ATCTGGTCAGTCGTGATTTCGCCCTTAATGTCGCTAAGGGACACCTTTCGCGTGTAGTG	2280	Db	3241 ATCTGGTCAGTCGTGATTTCGCCCTTAATGTCGCTAAGGGACACCTTTCGCGTGTAGTG
QY	2281	TCAAGATCTACGCCAGATGCCAGCTGGCAGGGCTCAAGAACCTGACCTTGCGTGTAGTG	2340	QY	
QY	2281	TCAAGATCTACGCCAGATGCCAGCTGGCAGGGCTCAAGAACCTGACCTTGCGTGTAGTG	2340	Db	3241 TCAAGATCTACGCCAGATGCCAGCTGGCAGGGCTCAAGAACCTGACCTTGCGTGTAGTG
QY	2341	ATTCCCTGAAAGGGTGAGATCATGTCGAGGCTCTGTGATTTACTGACTAGATGGGAACGGG	2400	QY	
QY	2341	ATTCCCTGAAAGGGTGAGATCATGTCGAGGCTCTGTGATTTACTGACTAGATGGGAACGGG	2400	Db	3241 ATTCCCTGAAAGGGTGAGATCATGTCGAGGCTCTGTGATTTACTGACTAGATGGGAACGGG
QY	2401	TGGCGCTGCTGCTGAGGACGACCTCTGTGATTTACTGACTAGATGGGAACGGG	2460	QY	
QY	2401	TGGCGCTGCTGCTGAGGACGACCTCTGTGATTTACTGACTAGATGGGAACGGG	2460	Db	3241 TGGCGCTGCTGCTGAGGACGACCTCTGTGATTTACTGACTAGATGGGAACGGG
QY	2461	ACCTCACACTGCTCTCGTGCACAGCTGGAGGACAAAGCAGCGAGGGGGCTTG	2520	QY	
QY	2461	ACCTCACACTGCTCTCGTGCACAGCTGGAGGACAAAGCAGCGAGGGGGCTTG	2520	Db	3241 ACCTCACACTGCTCTCGTGCACAGCTGGAGGACAAAGCAGCGAGGGGGCTTG
QY	2521	GGGACGGCAGGCTGGCCAGGGCCACACATCAGCTACCCATGCGTGTGCGT	2580	QY	
QY	2521	GGGACGGCAGGCTGGCCAGGGGCCACACATCAGCTACCCATGCGTGTGCGT	2580	Db	3241 GGGACGGCAGGCTGGCCAGGGGCCACACATCAGCTACCCATGCGTGTGCGT
QY	2581	CCCAGATCGCTCCGCATGGCTGCGACACTTGTGACATGGACCTGG	2640	QY	
QY	2581	CCCAGATCGCTCCGCATGGCTGCGACACTTGTGACATGGACCTGG	2640	Db	3241 CCCAGATCGCTCCGCATGGCTGCGACACTTGTGACATGGACCTGG
QY	2641	CCACCGGGAACTGCTCTAGTGGGAAATTTCACCATCAAATCGGAGCTTGCGATG	2700	QY	
QY	2641	CCACCGGGAACTGCTCTAGTGGGAAATTTCACCATCAAATCGGAGCTTGCGATG	2700	Db	3241 CCACCGGGAACTGCTCTAGTGGGAAATTTCACCATCAAATCGGAGCTTGCGATG
QY	2701	GCCGGACCTCTATCTCTGGGACTATTACCGTGTGCGAGGCGGGCAGTGTGCCATC	2760	QY	
QY	2701	GCCGGACCTCTATCTCTGGGACTATTACCGTGTGCGAGGCGGGCAGTGTGCCATC	2760	Db	3241 GCCGGACCTCTATCTCTGGGACTATTACCGTGTGCGAGGCGGGCAGTGTGCCATC
QY	2761	GCTGGATGCTCTGGGAGTCATCCCATGGAGACTTCAGCGACTCGAGCTGACGTGG	2820	QY	
QY	2761	GCTGGATGCTCTGGGAGTCATCCCATGGAGACTTCAGCGACTCGAGCTGACGTGG	2820	Db	3241 GCTGGATGCTCTGGGAGTCATCCCATGGAGACTTCAGCGACTCGAGCTGACGTGG
QY	2821	CCTTGGTGTGACCCCTGGAGGTGCTGATGCTCTGTAGGGCCAGCCCTTGGGAC	2880	QY	
QY	2821	CCTTGGTGTGACCCCTGGAGGTGCTGATGCTCTGTAGGGCCAGCCCTTGGGAC	2880	Db	3241 CCTTGGTGTGACCCCTGGAGGTGCTGATGCTCTGTAGGGCCAGCCCTTGGGAC
QY	2881	TCAACGACAGCAGGTATCGAGAACGCGGGGGTTCTCCGGACCCGGGGCAG	2940	QY	
QY	2881	TCAACGACAGCAGGTATCGAGAACGCGGGGGTTCTCCGGACCCGGGGCAG	2940	Db	3241 TCAACGACAGCAGGTATCGAGAACGCGGGGGTTCTCCGGACCCGGGGCAG
QY	2941	TGTTACCTGTCGCCGCCGCCAGGCCATATGACTGATGCTGGGT	3000	RESULT	2
QY	2941	TGTTACCTGTCGCCGCCGCCAGGCCATATGACTGATGCTGGGT	3000	A42378	
QY	3001	GGAGCCGGAGCTGAGCGACCCCTTCCAGGTGATGGTCTGCGAGG	3060	LOCUS	A42378
QY	3001	GGAGCCGGAGCTGAGCGACCCCTTCCAGGTGATGGTCTGCGAGG	3060	DEFINITION	A42378
QY	3061	ATGCACTACACAGGTGTGAATCACATCCACGCTGCGCCCTCTCAAGGACTGATCAG	3120	ACCESSION	A42378
QY	3061	ATGCACTACACAGGTGTGAATCACATCCACGCTGCGCCCTCTCAAGGACTGATCAG	3120	VERSION	A42378.1 GI:2297854
QY	3121	GGAGCTCAGCTTAATGAGGCACTAACAGAGACACATGGCACCTGGCCCTCCCTCCGA	3180	KEYWORDS	
QY	3121	GGAGCTCAGCTTAATGAGGCACTAACAGAGACACATGGCACCTGGCCCTCCCTCCGA	3180	SOURCE	unidentified
QY	3181	CAGCCCATCACCCTTAATGAGGCACTAACAGAGACACATGGCACCTGGCCCTCCCTCCGA	3240	ORGANISM	unclassified
QY	3181	CAGCCCATCACCCTTAATGAGGCACTAACAGAGACACATGGCACCTGGCCCTCCCTCCGA	3240	REFERENCE	1 (bases 1 to 3754)
QY	3181	CAGCCCATCACCCTTAATGAGGCACTAACAGAGACACATGGCACCTGGCCCTCCCTCCGA	3240	AUTHORS	Gusterson, B.A., Crompton, M.R., Mitchell, P.J., Barker, K.T., Martindale, J.E., Page, M.J. and Spence, P.
QY	3181	CAGCCCATCACCCTTAATGAGGCACTAACAGAGACACATGGCACCTGGCCCTCCCTCCGA	3240	TITLE	CELL GROWTH FACTOR RECEPTORS
QY	3241	CTGATGCCCTCTCCCTCTCCGACACTCTCGTGTGACCCAGGG	3300	COMMENT	Patent: WO 9502187-A 1 19-JAN-1995;
QY	3241	CTGATGCCCTCTCCCTCTCCGACACTCTCGTGTGACCCAGGG	3300	FEATURES	CANCER RES INST (GB) Other publication AU 7081094 950206.
QY	3241	CTGATGCCCTCTCCCTCTCCGACACTCTCGTGTGACCCAGGG	3300	FEATURES	1 . 3754 Location/Qualifiers
QY	3241	CTGATGCCCTCTCCCTCTCCGACACTCTCGTGTGACCCAGGG	3300	FEATURES	1 . 3754 /organism="unidentified"

QY	1918	CTTGGGCCAACCCACAAACCCAGGCTTACAGGGGACTATATGGAGCTGAGAAC	1977	Db
Db	1742	CTGGGCCAACCCACAAACCCAGGCTTACAGGGGACTATATGGAGCTGAGAAC	1801	QY
QY	1973	CAGGGCCCGCTCTGCCAACCTCCAGAACAGGCTTCTGGGACTATGGAGCTGAGAAC	2037	Db
Db	1862	CAGGGCCCGCTCTGCCAACCTCCAGAACAGGCTTCTGGGACTATGGAGCTGAGAAC	1861	QY
QY	2038	ACATGTTAACCTCCAGGGCTTACGGGAGAACACCAAGGGCTACAGGGGACTATGGAGCTGAGAAC	2097	Db
Db	1862	ACATGTTAACCTCCAGGGCTTACGGGAGAACACCAAGGGCTACAGGGGACTATGGAGCTGAGAAC	1921	QY
QY	2088	CAGGGCAGGGGATGGGCCCCAGGGGTTCTCGTGAACCTCCACTCGCTTCA	2157	Db
Db	1922	CAGGGCAGGGGATGGGCCCCAGGGGTTCTCGTGAACCTCCACTCGCTTCA	1981	QY
QY	2158	AGGAGAAGGCTTGGCGAGGGCCAGTTGGGAGGGACTCTGAGGCTGACAGGCC	2217	Db
Db	1982	AGGAGAAGGCTTGGCGAGGGCCAGTTGGGAGGGACTCTGAGGCTGACAGGCC	2041	QY
QY	2218	ANGATCTGTCAGTCTGATTTCCCTTAATGCGCTAAGGGACACCTTGTGGTAG	2277	Db
Db	2042	ANGATCTGTCAGTCTGATTTCCCTTAATGCGCTAAGGGACACCTTGTGGTAG	2101	QY
QY	2278	CGTCAAGATCTAGGCCAGATGCCAACAGATGCCAGCTTCTCTGTCTCCAGGA	2337	Db
Db	2102	CGTCAAGATCTAGGCCAGATGCCAACAGATGCCAGCTTCTCTGTCTCCAGGA	2143	QY
QY	2338	ATGATTCCTGAAAGGGTGAAGATCATGTCAGGCTCAAGGACCCACATCGC	2397	Db
Db	2144	ATGATTCCTGAAAGGGTGAAGATCATGTCAGGCTCAAGGACCCACATCGC	2203	QY
QY	2398	TCTGGCGCTGNGTGCAGGAGGACCCCTCTGCTAGTACTGACTCATGGAGAC	2457	Db
Db	2204	TCTGGCGCTGNGTGCAGGAGGACCCCTCTGCTAGTACTGACTCATGGAGAC	2263	QY
QY	2458	GCGACCTAACAGTCTCTAGGCCAACAGCTGGAGGACAGGCCAGGGGGCC	2517	Db
Db	2264	GCGACCTAACAGTCTCTAGGCCAACAGCTGGAGGACAGGCCAGGGGGCC	2323	QY
QY	2518	CTGGGGAGGGAGGTGCGAGGGCCACACTGGAGGACAGGCCAGGGGGCC	2577	Db
Db	2324	CTGGGGAGGGAGGTGCGAGGGCCACACTGGAGGACAGGCCAGGGGGCC	2383	QY
QY	2578	CAGCCCAGATGCCCTCGGCATGGCPATCTGCACACTCACTTGTACGGAC	2637	Db
Db	2384	CAGCCCAGATGCCCTCGGCATGGCPATCTGCACACTCACTTGTACGGAC	2443	QY
QY	2638	TGGCAGCGGAACTCTGCTCTGGGAATTACCATCAAAATGGAGCTTGGCA	2697	Db
Db	2444	TGGCAGCGGAACTCTGCTCTGGGAATTACCATCAAAATGGAGCTTGGCA	2503	QY
QY	2698	TGAGCGGAACTCTATGGGAATTACCATCAAAATGGAGCTTGGCA	2757	Db
Db	2504	TGAGCGGAACTCTATGGGAATTACCATCAAAATGGAGCTTGGCA	2563	QY
QY	2758	TCCGCTGATGGCTGGAGCTGCACTCTGGGAATTACCATCAAAATGGAGCTTGGCA	2817	Db
Db	2564	TCCGCTGATGGCTGGAGCTGCACTCTGGGAATTACCATCAAAATGGAGCTTGGCA	2623	QY
QY	2818	GGGGCTTGTGACGGGACTATACCGTGTGGAGGGCTGAGCTGCTGCCA	2877	Db
Db	2624	GGGGCTTGTGACGGGACTATACCGTGTGGAGGGCTGAGCTGCTGCCA	2683	QY
QY	2878	AGCTACCGACGAGGAGGATCGAGAACCGGGGGAGTCTTCGGGACAGGGCGGC	2937	Db
Db	2684	AGCTACCGACGAGGAGGATCGAGAACCGGGGGAGTCTTCGGGACAGGGCGGC	2743	QY
QY	2938	AGGTGACTCTGTCGGGGCCCTCTGGGAGGCTATGGAGCTGAGCTGCTGG	2997	Db
Db	2744	AGGTGACTCTGTCGGGGCCCTCTGGGAGGCTATGGAGCTGAGCTGCTGG	2803	QY
QY	2998	GCTGAGCGGGAGCTGAGCACGCCACCCCTTCCAGCTGATCGTCTGGAG	3057	Db
RESULT	3			
HUMNRK				
LOCUS				
DEFINITION	Homo sapiens receptor tyrosine kinase mRNA, complete cds.			
ACCESSION	L11315			
VERSION	L11315.1			
KEYWORDS	receptor tyrosine kinase,			
SOURCE	Homo sapiens (library: lambda-gt1) term placenta cDNA to mRNA.			
ORGANISM	Homo sapiens			

Db	1442 TGTCCCTCATGCTCTGGGGCTCACTGCGAGGCTCCTCGAAGCTGAGGGAGG	Db	2504 GCGGAACTCTATGCTGGGACTATTACGGTGTGAGGGGGCAAGCTGCCATCC
Qy	1681 TGTGGAGAGGAGGAGCTGCGGTCACCTCTGCTCCCTGGGACACTATCCATCAAC	Qy	2761 GCTGGATGGCCTGGGAGGTCATCCTCATGGGAAGTTACGACTGGGAGCTGGG
Db	1502 TGTGGAGAGGAGGAGCTGCGGTCACCTCTGCTCCCTGGGACACTATCCATCAAC	Db	2564 GCTGATGCGCTGGAGTCATCCTCATGGGAAGTTACGACTGGGAGCTGGG
Qy	1741 ACGGCCAGGTCCTAGAGAGCCACCCCGTAGAGGAGCCACCCCGTAGAGGAGC	Qy	2821 CCTTGGGTGACCTGTTGGAGGTCATGGAGTTACGACTGGGAGCTGGG
Db	1562 ACGCCAGGTCCTAGAGGAGCCACCCCGTAGAGGAGCCACCCCGTAGAGGAGC	Db	2624 CCTTGGGTGACCTGTTGGAGGTCATGGAGTTACGACTGGGAGCTGGG
Qy	1801 CCACACTCGCTCTGCTGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC	Qy	2881 TCGGAGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Db	1682 CCACACTCGCTCTGCTGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC	Db	1860 TCGGAGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Qy	1921 GGCCCAACCCACACCCAGGCTACAGTTGGGACTATGGACCCCTGAGAGGAGC	Qy	1980 GGACCGGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Db	1742 GGCCCAACCCACACCCAGGCTACAGTTGGGACTATGGACCCCTGAGAGGAGC	Db	1681 GGACCGGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Qy	1981 GGCCCCGCTTGCCGCACTCCAGGAGCTACAGTTGGGACTATGGACCCCTGAGAGGAGC	Qy	1920 GGACCGGGAGGTCAGAGGAGCCACCCCGTAGAGGAGCCACCCCGTAGAGGAGC
Db	1802 GGCCCCGCTTGCCGCACTCCAGGAGCTACAGTTGGGACTATGGACCCCTGAGAGGAGC	Db	1741 GGACCGGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Qy	2041 TTGTTACCTCGAGGAGCTCCAGGAGCTACAGTTGGGACTATGGACCCCTGAGAGGAGC	Qy	2040 GGACCGGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Db	1862 TTGTTACCTCGAGGAGCTCCAGGAGCTACAGTTGGGACTATGGACCCCTGAGAGGAGC	Db	1861 GGACCGGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Qy	2101 GGCGACTCGGGATGGCCCCAGGAGTTCTCGTCTCAGCTCGGTAAGG	Qy	2160 GGACCGGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Db	1922 GGCGACTCGGGATGGCCCCAGGAGTTCTCGTCTCAGCTCGGTAAGG	Db	1861 GGACCGGGAGGTCAGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Qy	2151 AGAACCTGGGAGGCCAGTTGGGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC	Qy	2101 AGAACCTGGGAGGCCAGTTGGGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Db	1982 AGAACCTGGGAGGCCAGTTGGGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC	Db	2041 AGAACCTGGGAGGCCAGTTGGGAGGAGCTGAGGAGCCACCCCGTAGAGGAGCCAC
Qy	2221 ATCTGGTCACTGCTGTTCCCTTAATGCGTAAAGGAGAACCTTGTGAGCTG	Qy	2220 ATCTGGTCACTGCTGTTCCCTTAATGCGTAAAGGAGAACCTTGTGAGCTG
Db	2042 ATCTGGTCACTGCTGTTCCCTTAATGCGTAAAGGAGAACCTTGTGAGCTG	Db	2041 ATCTGGTCACTGCTGTTCCCTTAATGCGTAAAGGAGAACCTTGTGAGCTG
Qy	2281 TCAAGATCTAGCCAGATGCCAACAGATGCCAGCTCTCTGTCAGGAT	Qy	2340 GCTGATGCCCTCTCCCTCTGAGGACACTCTGTCAGGAT
Db	2102 TCAAGATCTAGCCAGATGCCAACAGATGCCAGCTCTCTGTCAGGAT	Db	3180 ACAGCCCCATACCTCTAATAGGGAGCTGAGACTGCGGAGGAGCTGGGAGG
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Qy	2401 TGGGGTGTGTCAGGAGCACCCCTGCTGAGGAGCTGAGGAGCCGG	Qy	3199 ACAGCCCCATACCTCTAATAGGGAGCTGAGACTGCGGAGGAGCTGGGAGG
Db	2204 TGGGGTGTGTCAGGAGCACCCCTGCTGAGGAGCTGAGGAGCCGG	Db	3040 GCTGATGCCCTCTCCCTCTGAGGACACTCTGTCAGGAT
Qy	2461 ACCTCACCACTGCTGCTGAGGAGCACCCCTGCTGAGGAGCCGG	Qy	3200 CTAGAGCCCCCTGCCCCCTGAGGAGCTGCGGAGGAGCTGGGAGGAGCTGGGAGG
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Qy	2521 GGAGGGAGGAGGAGGAGGCCACATCTGAGGAGCTGAGGAGCCGG	Qy	3159 CTAGAGCCCCCTGCCCCCTGAGGAGCTGCGGAGGAGCTGGGAGGAGCTGGGAGG
Db	2324 GGAGGGAGGAGGAGGCCACATCTGAGGAGCTGAGGAGCCGG	Db	3360 TAGCCATCCTGGGGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG
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Qy	2701 CCCGGAGCTCTGCGGAGGAGCTGAGGAGCCGG	Qy	3279 GGACCACTGGGGCCACTGGCACACACTGAGGAGGAGCTGGGAGG
Db	2760 CCCGGAGCTCTGCGGAGGAGCTGAGGAGCCGG	Db	3420 GGACCACTGGGGCCACTGGCACACACTGAGGAGGAGCTGGGAGG
Qy	3539 GAAGGAGGAGAATGTTCTGAGGAGCTGGGAGGAGCTGGGAGG	Qy	3478 GGACCACTGGGGCCACTGGCACACACTGAGGAGGAGCTGGGAGG
Db	3340 GAAGGAGGAGAATGTTCTGAGGAGCTGGGAGGAGCTGGGAGG	Db	3220 GGACCACTGGGGCCACTGGCACACACTGAGGAGGAGCTGGGAGG
Qy	3599 TCTCTCTGTCACACTGGGAGGAGCTGGGAGGAGCTGGGAGG	Qy	3479 TCTCTCTGTCACACTGGGAGGAGCTGGGAGGAGCTGGGAGG
Db	3400 TCTCTCTGTCACACTGGGAGGAGCTGGGAGGAGCTGGGAGG	Db	3280 TCTCTCTGTCACACTGGGAGGAGCTGGGAGGAGCTGGGAGG
Qy	3658 CCCCACTTCACTGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG	Qy	3480 CCCCACTTCACTGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG
Db	3460 CCCCACTTCACTGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG	Db	3339 CCCCACTTCACTGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG
Qy	3718 GAGAAATTTGGGATGGGGAAAGAGGGAGGAGCTGGGAGGAGCTGGGAGG	Qy	3559 CCCCACTTCACTGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG
Db	3520 GAGAAATTTGGGATGGGGAAAGAGGGAGGAGCTGGGAGGAGCTGGGAGG	Db	3567 CCCCACTTCACTGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG
Qy	3778 ATCTCTAGGAGCTGGCCACATTTCTAATCTCTGGGTTGAGCTT	Qy	3579 CCCCACTTCACTGAGGAGCTGGGAGGAGCTGGGAGGAGCTGGGAGG
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RESULT	4	BC008716	BC008716	3849 bp	mRNA	linear	PRI 12-JUL-2001
LOCUS							
DEFINITION	Homo sapiens, discoidin domain receptor family, member 1, clone						
REFERENCE	MGC:8681 IMAGE:2964574 ¹						
AUTHORS	1 (bases 1 to 3849)						
TITLE	Strasberg,R.						
JOURNAL	Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA						
REMARK	NIH MGC Project URL: http://mgc.nci.nih.gov						
COMMENT	Contact: MGC help desk Email: cpabps-r@mail.nih.gov						
TISSUE	Procurement: ARCC						
PRODUCTION							
LIBRARY							
PREPARATION							
CDNA							
LIBRARY							
ARRAYED							
BY	The I.M.A.G.E. Consortium (IIML)						
SEQUENCING							
CENTER	NISC ²						
GAITHERSBURG							
MARYLAND							
WEB SITE	http://www.nisc.nih.gov/						
CONTACT	nisc_mgcncharr.nih.gov						
SHVERCHENKO	Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,						
BENJAMIN	B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,						
DEIRICH	Guan,X., Gupta,J., Ho,S.-L., Karlin,E., Legaspi,R.,						
LIM	Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,						
MCDOWELL	McDowell,J., Pearson,R., Snidder,B., Stantripop,S., Thomas,P.J.,						
TIANGSON	Tiengson,E.E., Touchnan,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,						
ZHANG	Zhang,L.-H. and Green,E.D.						
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium (IIML) at: http://image.IIML.gov							
Series: IRLA Plate: 1 Row: 0 Column: 24							
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 403386.							
Location/Qualifiers							
FEATURES							
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Qy	62	TGCTCTGGAGGCCCTCG	GACACCCG	AGGCC	CGCCCTCCCG	CGGCCCTCGGCTCC	G	121
Db	84	TGCTCTGGAGGCCCTCC	GACACCG	AGGCC	CGCCCTCCCG	CGGCCCTCGGCTCC	G	143
Qy	122	CGCTCTGTGCTCCCTCG	CCGCTCCCG	CGCCCG	CGCCCG	CGCCCG	G	181
Db	144	CGCTCTGTGCTCCCTCG	CCGCTCCCG	CGCCCG	CGCCCG	CGCCCG	G	203
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Db	204	CGGGGTTGAGGCCCTGG	TGCGGAG	AGACCG	ATGAG	GGSTGCTG	TGAGGGTGCT	263
Qy	242	CACTGAGCGAGGGGTG	AGCTTG	GGAGG	ATGCGA	GATGCCA	AGAGATGCTG	301
Db	264	CACTGAGCGAGGGGTG	AGCTTG	GGAGG	ATGCGA	GATGCCA	AGAGATGCTG	323
Qy	302	GCCGAGGGATCAGGAGCT	ATGGG	ACAGG	ATGCTCC	AGAGATGCTGCC	ACACCCCTAG	361
Db	324	GCCGAGGGATCAGGAGCT	ATGGG	ACAGG	ATGCTCC	AGAGATGCTGCC	ACACCCCTAG	383
Qy	362	GCTGGCAAGGGAGATGCT	GACATG	AGGGAG	ATTTGAT	CTCTGGC	AAAGTGCGCTATG	421
Db	384	GCTGGCAAGGGAGATGCT	GACATG	AGGGAG	ATTTGAT	CTCTGGC	AAAGTGCGCTATG	443
Qy	422	CCTGGCATCAGGACGGG	ACATCC	CAGAC	GTGAC	TCTCTG	TGCTCCAGCTCTGTC	481
Db	444	CCTGGCATCAGGACGGG	ACATCC	CAGAC	GTGAC	TCTCTG	TGCTCCAGCTCTGTC	503
Qy	482	AGATTCCACTGCCGCC	CAACGG	GGTGTG	AGACACTG	ACGGG	GATGGGCC	541
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Qy	542	CCCCGGAGGTGGTTC	CCAAGG	GGGGAG	TACTTG	CGAGGTG	ATACACCA	601
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Db	624	CCACCTGGCTCTGG	GGGACCCAGG	GGGACGG	CGATGCC	GGGGCTG	GGGAGG	683
Qy	662	CTCCGGAGGTGGTACT	CCGGCTGG	GGGAGG	TACTTG	CGAGGTG	ATACACCA	721
Db	684	CTCCGGAGGTACCGGCT	GGGAGG	TACTTG	CGAGGTG	ATACACCA	743	
Qy	722	CCGGTGGGGCAGGGAGT	GGTGTG	GGGAGG	TACTTG	CGAGGTG	ATACACCA	781
Db	744	CCGGTGGGGCAGGGAGT	GGTGTG	GGGAGG	TACTTG	CGAGGTG	ATACACCA	803
Qy	782	OCTTGGGCCCATGGT	GGCCGACT	GGGGTGTG	CGCTCTAC	CCCCGGCTG	ACGGGGTC	841

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3849)
 AUTHORS 1
 STRAUSBERG, R.
 TITLE Direct Submission
 JOURNAL Submitted (31-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabps@remail.nih.gov
 Tissue Procurement: ATCC
 DNA Library Preparation: Rubin laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
 URL: <http://www.systemsbiology.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
 Greene, Mark Kettman and Anuradha Madan
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium (LLNL) at: <http://image.llnl.gov>
 Series: IRLA Plate: 10 Row: f Column: 21
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 Best Local Similarity 95.9%; Pred. No. 0;
 Matches 3792; Conservative 0; Mismatches 31; Indels 130; Gaps 3;
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 ORIGIN
 RESULT 5
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 DEFINITION Homo sapiens, clone MGC:3909 IMAGE:2964574, mRNA, complete cds.
 ACCESSION BC013400
 VERSION BC013400.1 GI:15426562
 KEYWORDS MGC.
 SOURCE human.

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QY	782	CCTGGGCCCTCATGGTGCGACTGGTGTGCTCTACCCGGGTGACGGGTAT	841
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QY	842	GAGTCTGTCTGGGGTAGAGCTATGGCTATGGCTGCTCTGAGGGATGACTGTGCTA	901
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QY	1862	CCTCTCTGGCCACTTACGCCGTCCTCTGGGGCCGCCACCCCGCTG	1921
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QY	1922	GGCAAACCAACACCCAGGCTACAGTGGGACTATATGGCTCTGGAGAGGAG	1981
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QY	2042	TGTACCTCTGGGGCTACGGGGCAACCTGGGCTGGGCTGGGCTGGGCTGGG	2101
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QY	2102	GGCAGCGGGATGGGCCCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	2161
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QY	2162	GAAGCTGGGGCCAGTGGGAGGACCTGGGCTGGGCTGGGCTGGGCTGGG	2221
Db	2133	TCTGGTAACTCTGATTCCTCCCTTAATGGGGCAACCTGGGCTGGGCTGGG	2192
QY	2282	CAAGACTTACGGGGAGATGCCACAAAGATGCCAGCTCTCTCTGTCAGGATGA	2341

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QY	976	CCGTGGGGGAGCTGCAAGTATGGGGTCGGGCCAGCAGATGAGTGTTGGGGCTGG	1035
Db	737	CCGTGGGGAGCTGCAAGTATGGGGTCGGGCCAGCAGATGAGTGTTGGGGCTGG	796
QY	1036	ATGACTTAAAGGAGCTAGGGCTGGGGTGGGGATGACCTATGGGTGA	1095
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QY	1096	GCACACAGCTCCAGTGGCTAGGAGCTGGGGTGGGGTGGGGATGG	1155
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Db	917	CCITCCAGCTATGCACTGCACTGACACGCTGGGGTGGGGTGGGGCTGG	976
QY	1216	GGGGGGGAATGCTGTTCCGGCTGGCTGGCTGGCTGGGGGGAGGGCATGC	1275
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QY	1276	GCCACACCTAGGGGAACTTGGGACCCAGAGCCCCCTGTCTCAGTGCCCTG	1335
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QY	1336	GGGGCCTGTGCTCTGGCAAGCTGGGGACCCAGAGCCCCCTGTCTCAGTGCCCTG	1395
Db	1097	GGGGCCTGTGCTCTGGCAAGCTGGGGACCCAGAGCCCCCTGTCTCAGTGCCCTG	1156
QY	1396	TCAGC3AAATCTCTCATCTCTGAGTGGGACACATTCTCTGGGACTGGGCA	1455
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QY	1456	CCTCCGCCAGCCCCCTGGGGCCACTGGCCACACTCCACCACTTG	1515
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QY	1516	AGCTGAGCCAGGCCAGACATCTGCTTCCAGATTCACCTGGG	1575
Db	1277	AGCTGAGCCAGGCCAGACATCTGCTTCCAGATTCACCTGGG	1336
QY	1576	TCACTGGCTGCTGGGCCATCATCATCTGCTCTGTCATCATCTGCT	1635
Db	1337	TCACTGGCTGCTGGGCCATCATCATCTGCTCTGTCATCATCTGCT	1396
QY	1636	GGCGGGTGACTGGCCAGGGCTCTGAGCAGGGTGACGGAGGTGAGAAGGAGC	1655
Db	1397	GGCGGGTGACTGGCCAGGGCTCTGAGCAGGGTGACGGAGGTGAGAAGGAGC	1456
QY	1696	TGACGGTTACCTCTGCTCTGGGACACTATCTCATCACACCGCCAGCTCA	1755
Db	1457	TGACGGTTACCTCTGCTCTGGGACACTATCTCATCACACCGCCAGCTCA	1516
QY	1756	GAGGCCACCCCGTACAGGAGCCGGCTCTGAGCAGGGTGACGGAGGTGAGAAGGAGC	1815
Db	1517	GAGGCCACCCCGTACAGGAGCCGGCTCTGAGCAGGGTGACGGAGGTGAGAAGGAGC	1576
QY	1816	GTGTCCTCAATGGCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	1875
Db	1577	GTGTCCTCAATGGCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	1636

QY	1876	CTTACCCCGTCCCCCTCGAGGGGGCCCCCACCCGCCCTGGGCCAACCCACCA	1935	QY	2956	CGCCCTGCCCTCCCCGGAGGCTTATGAGCTGATCTGGCTGGCTGGAGCTG	3015
Db	1637	CTTACGCCGCTCCCTCGAGGCCGGCCCCCACCCGCCCTGGGCCAACCCACCA	1996	Db	2699	CGCCCTGCCCTCCCCGGAGGCTTATGAGCTGATCTGGCTGGCTGGAGCTG	2758
QY	1936	ACACCCAGGGCTACAGTGGGAGCTATATGAGGAGCTGAGAGCAGGCCCTCTGC	1995	QY	3016	AGCACCGACACCCCTTCCAGCTGATGGCTGGCTGGAGCTAACACCG	3075
Db	1697	ACACCCAGGGCTACAGTGGGAGCTATATGAGGAGCTGAGAGCAGGCCCTCTGC	1756	Db	2759	AGCACCGACACCCCTTCCAGCTGATGGCTGGCTGGAGCTAACACCG	2818
QY	1996	CCCCACCTCCCGAGACAGCGCTCCCTGAGGAGCTGAGAGCAGGCCCTCTGC	2055	QY	3076	TGTGATCATCACATCGTGGCTCTGGAGGATATCCAGGGAGCTGAGCA	3135
Db	1757	CCCCACCTCCCGAGACAGCGCTCCCTGAGGAGCTGAGAGCAGGCCCTCTGC	1816	Db	2819	TGTGATCATCACATCGTGGCTCTGGAGGATATCCAGGGAGCTGAGCA	2878
QY	2056	GGGTGACCCGGGGGCACACCTATGCTGAGCTGAGCTGAGGAGCTGGGATG	2115	QY	3135	CTAAACAGAGGACACATGGCACCTCTCCCTCCCTCCAGGGAGTGGGAG	3195
Db	1817	GGGTGACCCGGGGGCACACCTATGCTGAGCTGAGCTGAGGAGCTGGGATG	1876	Db	2879	CTAAACAGAGGACACATGGCACCTCTCCCTCCAGGGAGTGGGAG	2938
QY	2116	GGCCCCCAGAGTGGGATTCCTCGATCTGAGCTGAGGAGCTGGGAG	2175	QY	3195	AATAGAGGAGTGGAGCTGAGGAGCTGGGAGTGGGAGCTGAGGAG	3255
Db	1877	GGCCCCCAGAGTGGGATTCCTCGATCTGAGGAGCTGGGAG	1936	QY	3255	CCCTTCTGACACACTCTCATGTCCTCTCCCTCCAGGGAGCTGAGGAG	3315
QY	2176	GCACATTGGGGAGSTGAGCTGAGCTGAGGAGCTGGGAG	2235	Db	2939	AATAGAGGAGTGGAGACTGC-----AGAGCCCTCTGC	2958
Db	1937	GCACATTGGGGAGSTGAGCTGAGGAGCTGGGAG	1996	Db	2959	-----AGAGCCCTCTGC-----AGAGCCCTCTGC	2972
QY	2236	ATTTCCCCCTAATGTCGTAAGGACACCTTGTGTTAGCTGAGATCTACGC	2295	QY	3315	CCACCCACACTGGCTCTGGAGGGACTCTTCACCTCTCTAGGATCCCTGGG	3375
Db	1997	ATTTCCCCCTAATGTCGTAAGGACACCTTGTGTTAGCTGAGATCTACGC	2056	Db	2973	CCACCCACACTGGCTCTGGAGGGACTCTTCACCTCTCTAGGATCCCTGGG	3032
QY	2296	CAGATGCCACCAAGAATGGCAGCTCTCTGCTCCAGGATGATTCTCAGAAG	2355	QY	3376	AAGGGGGAGAATATGGATAGACAGCTGGGAGATGGGACCTGGGCCC	3435
Db	2057	CAGATGCCACCAAGAATGGCAGCTCTCTGCTCCAGGATGATTCTCAGAAG	2098	Db	3033	AAGGGGGAGAATATGGATAGACAGCTGGGAGATGGGACCTGGGCCC	3092
QY	2356	TGAAGATCATGTCAGGGCTCAAGGACCCACATCTGGCTCTGGGAG	2415	QY	3436	ACTGGACACACATGATCTGGAGGGCTGCTGGGCTGCTGGTC	3494
Db	2099	TGAAGATCATGTCAGGGCTCAAGGACCCACATCTGGCTCTGGGAG	2158	Db	3093	ACTGGACACACATGTCAGGGCTGCTGGGAGGGCTGCTGGGAG	3152
QY	2416	AGGACGACCCCTCTGCAATGATGACTGACTACATGGAGACAGCTGCC	2475	QY	3495	ACATGGACACCACTGGCTGGAGAATCTGGGGAGGGAGACAGAAGGAGAATG	3554
Db	2159	AGGACGACCCCTCTGCAATGATGACTGACTACATGGAGACAGCTGCC	2218	Db	3153	ACATGGACACCACTGGCTGGAGAATCTGGGGAGGGAGACAGAAGGAGAATG	3212
QY	2476	TCACTGCCACCCCTCTGGAGGACAGGGAGCCAGGGAGCCCTGGGACGGCAGGTG	2535	QY	3555	TTCTCTGGCCCTCTCTGCTACTCTGTCAGCTGGGCTCTCCCTCCATCAGCT	3614
Db	2219	TCACTGCCACCCCTCTGGAGGACAGGGAGCCAGGGAGCCCTGGGACGGCAGGTG	2278	Db	3213	TTCTCTGGCCCTCTCTGCTACTCTGTCAGCTGGGCTCTCCCTCCATCAGCT	3272
QY	2536	CGCAGGGGCCACCATCAGCTGAGGACAGGGAGCCCTGGGACGGCAGGTG	2595	QY	3615	GAACACTGGACCTGGGGTAGGCCAGGGAGATGGCTCG	3674
Db	2279	CGCAGGGGCCACCATCAGCTGAGGACAGGGAGCCCTGGGACGGCAGGTG	2338	Db	3273	GAACACTGGACCTGGGGTAGGCCAGGGAGATGGCTCG	3332
QY	2596	GCATGCGCTATCTGCGACACTGACTCTGAGCTATGCGACCTGCG	2655	QY	3675	CAGCTGAGCTGAGACTCTCTAAGCTTACGCTTCTGGAGTAAATATGGGAT	3734
Db	2339	GCATGCGCTATCTGCGACACTGACTCTGAGCTATGCGACCTGCG	2398	Db	3333	CAGCTGAGCTGAGACTCTCTAAGCTTACGCTTCTGGAGTAAATATGGGAT	3392
QY	2656	TAGTGGGAAATTCAACATCAAATGCGACACTTGGCTGGGGAACTCTGATG	2715	QY	3757	GGGGGAGAGGGAGCAAGGCCCATAGGCTTGGGGTGGACATCTAGCTGAGCT	3794
Db	2399	TAGTGGGAAATTCAACATCAAATGCGACACTTGGCTGGGGAACTCTGATG	2458	Db	3393	GGGGGAGAGGGAGCAAGGCCCATAGGCTTGGGGTGGACATCTAGCTGAGCT	3452
QY	2716	CTGGGACTATACCGTGTGGAGTGTACGACTGCGGAGCTGGCTGGCTGG	2775	QY	3795	CACATGTTCTATACACTGGGGTGTACATGCTTGGGGAGAGACAGCT	3854
Db	2459	CTGGGACTATACCGTGTGGAGTGTACGACTGCGGAGCTGGCTGGCTGG	2518	Db	3453	CACATGTTCTATACACTGGGGTGTACATGCTTGGGGAGAGACAGCT	3512
QY	2836	TGGGGAGGTGCTGAGTGTGGAGGCCCCCTGGGAGCTACCGAGGAGG	2895	QY	3855	TTTACACATATGGACCTACTGGGGAGCTTACGCTTGGGGAGAGACAGCT	3914
Db	2579	TGGGGAGGTGCTGAGTGTGGAGGCCCCCTGGGAGCTACCGAGGAG	2638	Db	3513	TTTACACATATGGACCTACTGGGGTGTACATGCTTGGGGAGAGACAGCT	3572
QY	2896	TCTTCGAGAACGGGGGGAGTCTTCGGGACAGGGCCCTGGGAGCTACCG	2955	QY	3915	ATATAAAGGTGAGTTTCCACAAAAAA	3953
Db	2639	TCTTCGAGAACGGGGGGAGTCTTCGGGACAGGGCCCTGGGAGCTACCG	2698	Db	3573	ATATAAAGGTGAGTTTCCACAAAAAA	3611

RESULT 8

AR103004

LOCUS AR103004

DEFINITION Sequence 3 from patent US 6087144.

3637 bp DNA

Linear

PAT 14-FEB-2001

Best Local Similarity	97.0%	Pred.	No. 0;	Matches	3589;	Conservative	0;	Mismatches	5;	Indels	105;	gaps	3;																																																																																																											
QY	256	GTGCACTTGAGGAATGCCAAGAGATGCTGCCACCCCTTGGCCGGGGATCAG	315	Db	17	GTGCACTTGAGGAATGCCAAGAGATGCTGCCACCCCTTGGCCGGGGATCAG	76	QY	316	GAGCTATGGGACAGAGGGCTGTCATCTTAATCTGCTGCTCTGGGCAAGTGG	375	Db	77	GAGCTATGGGACAGAGGGCTGTCATCTTAATCTGCTGCTCTGGGCAAGTGG	136	I	QY	376	ATGCTGACATGAGGACATTTGATCCGCCAAGTGGCCCTATGCCCTGGCATGC	435	Db	137	ATGCTGACATGAGGACATTTGATCCGCCAAGTGGCCCTATGCCCTGGCATGC	196	QY	436	ACCGGACCATCCAGACAGTGCAGTCCTCTCTCCAGCTTCAGCTGGTGCAG	495	Db	197	ACCGGACCATCCAGACAGTGCAGTCCTCTCTCCAGCTTCAGCTGGTGCAG	256	QY	556	TGTTTCCCAAGGGGAGGGTACTCTGATCTGAGCTCCACCTGGTGGCTC	615	Db	317	TGTTTCCCAAGGGGAGGGTACTCTGATCTGAGCTCCACCTGGTGGCTC	376	QY	616	TGTTGGGACCCGGGACGGCAGCCGGCTGGGCAAGGAGTCTCGGAGCTAC	675	Db	377	TGTTGGGACCCGGGACGGCAGCCGGCTGGGCAAGGAGTCTCGGAGCTAC	316	QY	736	AGTTGATCTAGGCAATGGGACCTGGGATCTGGGACCTGGGCTGGGCCCCCA	795	Db	497	AGTTGATCTAGGCAATGGGACCTGGGATCTGGGACCTGGGCTGGGCCCCCA	556	QY	856	GGGTAGAGCTCTGGCTGCTGGGATGACTCTGTGTTACCGCCCTGTC	915	Db	617	GGGTAGAGCTCTGGCTGCTGGGATGACTCTGTGTTACCGCCCTGTC	676	QY	916	GGAGACAGTGTATTATCTGAGGCCGTTGGGGTGTGGCTACCTGAGGACATA	975	Db	677	GGAGACAGTGTATTATCTGAGGCCGTTGGGGTGTGGCTACCTGAGGACATA	736	QY	976	CGGTGGGGACTGTGAGTGGGTGTGGCCAGCTGAGCTGAGGACATGAGGACATA	1035	Db	737	CGGTGGGGACTGTGAGTGGGTGTGGCCAGCTGAGTGGGTGTGGGCTGG	796	QY	1036	ATGACTTGTAGGAGTCAGGGCTGGGGCTGGCCAGGTAGCTATGGGATGGA	1095	Db	797	ATGACTTGTAGGAGTCAGGGCTGGGGCTGGCCAGGTAGCTATGGGATGGA	856	QY	1096	GCACACACAGCTCTCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGG	1155	Db	857	GCACACACAGCTCTCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGG	916	QY	1156	CCTTCCAGGCTAGTCAGTGGCTAGGAGCTGGCTAGGAGCTGGCTAGG	1215	Db	917	CCTTCCAGGCTAGTCAGTGGCTAGGAGCTGGCTAGGAGCTGGCTAGG	976	QY	1216	GGGGGGGAATGTCGCTCCGGCTGGCCATGGCTGGGGGGCCATGC	1275	Db	977	GGGGGGGAATGTCGCTCCGGCTGGCCATGGCTGGGGGGCCATGC	1036	QY	1276	GCACACACAGCTAGGGGAAACCTGGGGACCCAGAGGCCGCGCTGTC	1335	Db	2099	TGAGATCATGTGAGGCTCAAGGACCCAAACATCATCGCTGCTGGCTGG	2158

Db	1037	GCCACAACTAGGGGAACTGGGGGACAGGCCGCGCTCTCAGTGCCTTG	1096
QY	1336	GGGGCGTGTGGCTCTTCTGCTGAGCTGGCTCTTCTGCTGCTGCTGCTG	1355
Db	1097	GGGGCGTGTGGCTCTTCTGCTGAGCTGGCTCTTCTGCTGCTGCTG	1156
QY	1396	TCAGGAAATCTCTTCATCTCTGATGTGGTGAACATTCCTCTGGGACTGGG	1455
Db	1157	TCAGGAAATCTCTTCATCTCTGATGTGGTGAACATTCCTCTGGGACTGGG	1216
QY	1456	CCTCCGGCCAGCCCTGTTGGGGCTGGCCACCTCCACCAACTCAGCAGCTG	1515
Db	1217	CCTCCGGCCAGCCCTGTTGGGGCTGGCCACCTCCACCAACTCAGCAGCTG	1276
QY	1516	AGCTGGAGCCAGGAGGCCAGGGCTGGCCAAAGGCCAGGGAGCCGACCCATC	1575
Db	1337	TCACGGCTACCTCTTCATCTGATGAGCTGGCTGAGCTGACCTGAGCT	1396
I	1277	ACCTGGAGCCAGGAGGCCAGGGCTGGGGCTGGCCAGGGTCTGGCTGG	1336
QY	1635	GCGGCTGCACTGGGAGGGCTCTGAGGCCGCGCTGGCCAGGGTCTCCGAGCT	1695
Db	1397	GGCGCTGCACTGGGAGGGCTCTGAGGCCGCGCTGGCCAGGGTCTCCGAGCT	1456
QY	1696	TGACGCTTACCTCTGTCGCTGGGAGACTATCTCTCATCACACCCAGTC	1755
Db	1457	TGACGCTTACCTCTGTCGCTGGGAGACTATCTCTCATCACACCCAGTC	1516
QY	1756	GAGGCCACCCGGTACCGAGGCCGCGCTGGGAGATCCGCCCTCTGCTCT	1815
Db	1517	GAGGCCACCCGGTACCGAGGCCGCGCTGGGAGATCCGCCCTCTGCTCT	1576
QY	1816	GTGTCCTCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1875
Db	1577	GTGTCCTCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1636
QY	1876	CTTAGGCCCTCCCTCTGAGGCCGCGCTGGGAGATCCGCCCTCTGCTCT	1935
Db	1697	ACACCCAGGCTACAGTGGGGACTATATGGAGCTGAGGAGCTGAGGAGCT	1756
QY	1995	CCCCACCTCCAGAACACGGCTCCCATATGGAGCTGAGGAGCTGAGATG	2055
Db	1637	CTTAGGCCCTCCCTCTGAGGCCGCGCTGGGAGATCCGCCCTCTGCTCT	1696
QY	1936	ACACCCAGGCTACAGTGGGGACTATATGGAGCTGAGGAGCTGAGGAGCT	1995
Db	1697	ACACCCAGGCTACAGTGGGGACTATATGGAGCTGAGGAGCTGAGGAGCT	1756
QY	2055	GGGTACCGGGGACACCGCTGAGCTGAGCTGAGGAGCTGAGCTGAGGAGCT	2115
Db	1817	GGGTACCGGGGACACCGCTGAGCTGAGCTGAGGAGCTGAGCTGAGGAGCT	1876
QY	2116	GGCCCCAGAGGTGGATTCTCTGATCTGAGCTGGCTCTGGAGAGCTGG	2175
Db	1877	GGCCCCAGAGGTGGATTCTCTGATCTGAGCTGGCTCTGGAGAGCTGG	1936
QY	2176	GCGTACCGGGGACACCGCTGAGCTGAGCTGAGGAGCTGAGCTGAGGAGCT	2235
Db	1937	GCGTACCGGGGACACCGCTGAGCTGAGCTGGCTCTGGAGAGCTGG	1996
QY	2226	ATTCCTCTTAATGTGGCTAGGACACCTCTGGAGCTGAGCTGAGCTGAGG	2295
Db	2057	CAGTCACCAAGAATGCTGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGG	2098
QY	2356	TGAGATCATGTGAGGCTCAAGGACCCAAACATCATCGCTGCTGGCTG	2415
Db	2099	TGAGATCATGTGAGGCTCAAGGACCCAAACATCATCGCTGCTGGCTG	2158

QY	2416	AGGACGACCCCTCTCGCAATGATCTGACTACTGAGAACGCGGACCTCACCGATTC	2475	QY	3495	ACACTGGACCCACTTGCTCAGAATCTGGGGTGGAGGACAAAGAAGGAGAAATG	3554				
Db	2159	AGGAGGACCCCTCTCGCAATGATCTGACTACTGAGAACGCGGACCTCACCGATTC	2218	Db	3113	ACACTGGACCCACTTGCTCAGAATCTGGGGTGGAGGACAAAGAAGGAGAAATG	3212				
QY	2476	TCACTGGCCACCCAGCTGGAGAACAGAGCCAGGGGGCCCTGGGAGGGGGAGGG	2355	QY	3555	TTCCCTTGAGCTGCTCCCTGACTCTGCTCAGCTGGCTCTCCCTCCCTCACCT	3614				
Db	2219	TCACTGGCCACCCAGCTGGAGAACAGAGCCAGGGGGCCCTGGGAGGGGGAGGG	2278	Db	3213	TTCCCTTGAGCTGCTCCCTGACTCTGCTCAGCTGGCTCTCCCTCCCTCACCT	3272				
QY	2536	CGCAGGGGCCACCACTCAGCTTACCCAACTGCTGCGATCTGGAGCCAGATGCTC	295	QY	3615	GAACACTGACCTGGGSPAGCCGCCAGCCTGAGCTACCCCTCTCCACTG	3674				
Db	2279	CGCAGGGGCCACCACTCAGCTTACCCAACTGCTGCGATCTGGAGCCAGATGCTC	2338	Db	3273	GAACACTGACCTGGGSPAGCCGCCAGCCTGAGCTACCCCTCTCCACTG	3332				
QY	2596	GCATGGCCTATCTGGCACACTCACTTGACATCGGACCTGGGGAACTG	2655	QY	3675	CAGCTTGAGCTGAGACTCTCTAGCTTACCTTGTGGAGTAATATTGGAT	3734				
Db	2339	GCATGGCCTATCTGGCACACTCACTTGACATCGGACCTGGGGAACTG	2398	Db	3333	CAGCTTGAGCTGAGACTCTCTAGCTTACCTTGTGGAGTAATATTGGAT	3392				
QY	2656	TAGTGGGGAAATTTCACCATCAGAACATGCGAGACTTGGCATAGCCGAACTCT	2715	QY	3735	GGGGGAAGAGGGGACACGGCCATACGCTTGGGCTTGGGACACTCT	3794				
Db	2399	TAGTGGGGAAATTTCACCATCAGAACATGCGAGACTTGGCATAGCCGAACTCT	2458	Db	3393	GGGGGAAGAGGGGACACGGCCATACGCTTGGGCTTGGGACACTCT	3452				
QY	2716	CTGGGAGACTATTACCGTGCAGGGCAGGGCCAGCCTTGGGACCTACCGAGAGCAG	2775	QY	3795	CACATTGATTTCTATACTACTTGGSPTGACATTGGGGGAGACAGT	3854				
Db	2459	CTGGGAGACTATTACCGTGCAGGGCAGGGCCAGGCTGATGCTGG	2518	Db	3453	CACATTGATTTCTATACTACTTGGSPTGACATTGGGGGAGACAGT	3512				
QY	2776	AGTSCATCCATGGGAAGTCACTGAGCTGCGGTGACCTGGGACTCTGG	2835	QY	3855	TTTACACTATATGGACTCTGTTGAGCTTACCTTGGSPTGACATTGGGGGAGACAGT	3914				
Db	2519	AGTSCATCCATGGGAAGTCACTGAGCTGACGCTGCGGTGACCTGG	2578	Db	3513	TTTACACTATATGGACTCTGTTGAGCTTACCTTGGSPTGACATTGGGGGAGACAGT	3572				
QY	2836	TGTGGGAGACTATTACCGTGCAGGGCAGGGCCAGGCTTGGGACCTACCGAGAGCAG	2895	QY	3915	ATAATAAGGTGAGTTCCACAAAAAAAGAAAAAA	3953				
Db	2579	TGTGGGAGACTATTACCGTGCAGGGCAGGGCCAGGCTTGGGACCTACCGAGG	2638	Db	3573	ATAATAAGGTGAGTTCCACAAAAAAAGAAAAAA	3611				
QY	2896	TGATCGAGAACGCGGGGAGTTCCACTGATCGGTCTGGCAGGGAGCTACCGC	2955	RESULT	10						
Db	2639	TGATCGAGAACGCGGGGAGTTCCACTGATCGGTCTGGCAGGGAGCTACCGC	2698	18045.							
QY	2956	CGCCCTGGCCGGCCAGGGCTATATGAGCTGCTGGGCTCTGGGAGGACTCTG	3015	LOCUS	180845						
Db	2699	CGCCCTGGCCGGCCAGGGCTATATGAGCTGCTGGGCTCTGGGAGGACTCTG	2758	DEFINITION	Sequence 3 from patent US 5709858.						
QY	3016	AGCAGCGACCCCTTCCAGGACAGGGCCAGGGGGAGCTGACTAACAGG	3075	ACCESSION	180845						
Db	2759	AGCAGCGACCCCTTCCAGGACAGGGCCAGGGGGAGCTGACTAACAGG	2818	VERSION	180845.1						
QY	3076	TGTGATCACACACCCAGCTGCCCTCCTCAGGAGTCAAGGAGCACTG	3135	KEYWORDS	GI:3209135						
Db	2819	TGTGATCACACACCCAGCTGCCCTCCTCAGGAGTCAAGGAGCACTG	2878	SOURCE	Unknown.						
QY	3136	CTAAACAAAGGACACACTTCCACTGATGGACCTCTGGGACCTACCT	3195	ORGANISM	Unclassified.						
Db	2879	CTAAACAAAGGACACACTTCCACTGATGGACCTCTGGGACCTACCT	2938	REFERENCE	1 (bases 1 to 3637)						
QY	3196	ATTAAGGAGTGGAGACTGGAGCTGGGGGGGGGACCCAGGGAGCTATGCC	3255	AUTHORS	Godowski, P.J., Mark, M.R. and Scadden, D.T.						
Db	2939	ATTAAGGAGTGGAGACTGGGGGGGGGACCCAGGGAGCTATGCC	2958	TITLE	Antibodies specific for Re receptor protein tyrosine kinase						
QY	3256	CCCTCTCTGGACACACTTCCATGAGCCCTTCCCTCCAGGCCATACCT	3315	JOURNAL	Patent: US 5709858-A 3 20-JAN-1998;						
Db	2959	CCCTCTCTGGACACACTTCCATGAGCCCTTCCCTCCAGGCCATACCT	2972	FEATURES	Location/Qualifiers						
QY	3316	CCACCCAGCTGCTCCCTGGGAGCTCTCCACCCCTCTAGGCCCCCTAGGCCCC	3375	source	1. .3637						
Db	2973	CCACCCAGCTGCTCCCTGGGAGCTCTCCACCCCTCTAGGCCATACCT	3032	BASE COUNT	1/organism="unknown"						
QY	3376	AAAGCTGGAGAAATAGGATAGACCTGGCATGGCCATGGGACCTGGGCC	3435	ORIGIN	1. .3637						
Db	3033	AAAGCTGGAGAAATAGGATAGACCTGGCATGGCCATGGGACCTGGGCC	3092	Query Match	87.1%; Score 3451; DB 6; Length 3637;						
QY	3436	ACTGGACACACTGATCTGGAGGGCTCG-CGCCAGCTCTCCCTGTCA	3494	Best Local Similarity	97.0%; Pred. No. 0;						
Db	3093	ACTGGACACACTGATCTGGAGGGCTCG-CGCCAGCTCTCCCTGTCA	3152	Matches	0; Mismatches						
QY	3495	ACGGACCATCCCAGACAGCTCTGCTTCAGCTCTGCTCAGATCCACTGCC	495	QY	256	GTGGACTCTGAGAACGCTGCTCAGAGATGCTGGCCCTAGGCCCC	315	Db	17	GTGGACTCTGAGAACGCTGCTCAGAGATGCTGGCCCTAGGCCCC	76
Db	3113	ACACTGGACCCACTTGCTCAGAATCTGGGGTGGAGGACAAAGAAGGAAATG	3212	QY	316	GACCTATGGAGGAGGGCCCTGCTCAGATGCTGGCTCTGGGAGCTG	375	Db	77	GACCTATGGAGGAGGGCCCTGCTCAGATGCTGGCTCTGGGAGCTG	136
QY	3555	TTCCCTTGAGCTGCTCCCTGACTCTGCTCAGCTGGCTCTCCCTCACCT	3614	QY	376	ATGCTGACATGAAGGGACATTTGATCTGCTGGCTATGCCATGAGGAG	435	Db	137	ATGCTGACATGAAGGGACATTTGATCTGCTGGCTATGCCATGAGGAG	196
Db	3213	TTCCCTTGAGCTGCTCCCTGACTCTGCTCAGCTGGCTCTCCCTCACCT	3272	QY	436	ACGGACCATCCCAGACAGCTCTGCTTCAGCTCTGCTCAGATCCACTGCC	495	Db	197	ACGGACCATCCCAGACAGCTCTGCTTCAGCTCTGCTCAGATCCACTGCC	256

Db	2399	TAGTGGCCAAATTTCACATCAAATGCCAAGTCGCACTTGTGGGGGACCTCTTG	2458
Qy	2716	CTGGGGACTTACCGTGTGAGGGCGGGCAGTGTGCCCATCGCCTGGATGCGCTGG	2775
Db	2459	CTGGGGACTTACCGTGTGAGGGCGGGCAGTGTGCCCATCGCCTGGATGCGCTGG	2518
Qy	2776	AGTCATCTCATGGGAGTCAGACTGCTGAGGCACTGAGCTGAGTGGCTTGTG	2835
Db	2519	AGTCATCTCATGGGAGTCAGACTGCTGAGGCACTGAGCTGAGTGGCTTGTG	2578
Qy	2836	TGTTGGGGACTGCTGATGCTGAGGCACTGAGCTGAGTGGCTTGTG	2895
Db	2579	TGTTGGGGACTGCTGATGCTGAGGCACTGAGCTGAGTGGCTTGTG	2638
Qy	2896	TCATCGAACCGGGGAGTCGGACAGGGCCGGAGGTACCGTCTCCCGC	2955
Db	2839	TCATCGAACCGGGGAGTCGGACAGGGCCGGAGGTACCGTCTCCCGC	2698
Qy	2956	CGCTGCTGCCGAGGGCTATAGACGCTGAGCCTGGCTGGAGGGAGTG	3015
Db	2699	CGCTGCTGCCGAGGGCTATAGACGCTGAGCCTGGCTGGAGGGAGTG	2758
Qy	3016	AGCGGACACCCCTTCCAGCTGATGCTGAGGAGCACTAACCG	3075
Db	2759	AGAGGACACCCCTTCCAGCTGATGCTGAGGAGCACTAACCG	2818
Qy	3076	TGTAATCACATCCAGTGCCTCCCTCAGGAGTGTCCAGGGAGCAGACA	3135
Db	2819	TGTAATCACATCCAGTGCCTCCCTCAGGAGTGTCCAGGGAGCAGACA	2878
Qy	3136	CTAAACAGGAGACAAAGGACCTGTGCCTTCCTCCGACGCCACACT	3195
Db	2879	CTAAACAGGAGACAAAGGACCTGTGCCTTCCTCCGACGCCACACT	2938
Qy	3196	ATATGAGGAGAGACTGCAAGTGGCTGSCCCACCCAGGAGCTGATGCC	3255
Db	2939	ATATGAGGAGAGACTGCAAGTGGCTGSCCCACCCAGGAGCTGATGCC	2958
Qy	3256	CCCTCCGTGACACACTCTATGTCCTTCCTAGAAGCCCTG	3315
Db	2959	CCCTCCGTGACACACTCTATGTCCTTCCTAGAAGCCCTG	3315
Qy	3316	CCACCCAGCTGGCTGGGAGGACCTCCACCCCTAGCCATCCCTGGG	3375
Db	2973	CCACCCAGCTGGCTGGGAGGACCTCCACCCCTAGCCATCCCTGGG	3032
Qy	3376	AAGGGTGGGAGAAATAGATAGACGACATGGACATGGCCCATGGACCTGG	3435
Db	3033	AAGGGTGGGAGAAATAGATAGACGACATGGACATGGCCCATGGACCTGG	3092
Qy	3436	ACTGGACAACTGTCTGGAGGTGCTGG-CCCAGCTCTCTCCCTGTCAC	3494
Db	3093	ACTGGACAACTGTCTGGAGGTGCTGG-CCCAGCTCTCTCCCTGTCAC	3152
Qy	3495	ACACTGACCCACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3554
Db	3153	ACACTGACCCACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3212
Qy	3555	TTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3614
Db	3213	TTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3272
Qy	3615	GAACACTGACCTGGGTAGCCCACTGAGCTCTAAGCTACGTTCTG	3674
Db	3273	GAACACTGACCTGGGTAGCCCACTGAGCTCTAAGCTACGTTCTG	3332
Qy	3675	CACTGCTGACTGACTCTAAGCTACGTTCTGAGGAGGAGGAGGAGG	3734
Db	3333	CACTGCTGACTGACTCTAAGCTACGTTCTGAGGAGGAGGAGGAGG	3392
Qy	3735	GGGGGAACAGGGCAAGGCCATAGCCTGGGTGAGCAGCTGAGTC	3794
Qy	3795	CACATGATTTCTAATCACTGCGGTTGCAATTGCGGGAGACAGAT	3854
Db	3453	CACATGATTTCTAATCACTGCGGTTGCGGTTGCAATTGCGGGAGACAGAT	3512
Qy	3855	TTCACATATAGGACTAGGTGAGCAATTAACTCCGACTAGGCC	3914
Db	3513	TTCACATATAGGACTAGGTGAGCAATTAACTCCGACTAGGCC	3572
Qy	3915	ATATAAAGGTGAGTTTACACAAAAAA	3953
Db	3573	ATATAAAGGTGAGTTTACACAAAAAA	3611
RESULT 11			
REFERENCE	AX268594	AX268594	AX268594
AUTHORS	1 (sites)	Sequence 13	from Patent. WO175404.
PRATT,J.Y.,	Cochran,S.W.,	Paterson,G.Y.,	Ohashi,Y.W., Morris,B.Y. and
TITLE	Schizophrenia related genes	PATENT	WO 0175404-A 13 11-OCT-2001;
JOURNAL	WELFIDE CORPORATION (JP)	LINEAR	
FEATURES	Location/Qualifiers	PAT	29-OCT-2001
SOURCE	1. .3554 /organism="Homo sapiens"		
BASE COUNT	682 a 1064 c 1065 g 743 t		
ORIGIN			
Query Match			
Best Local Similarity	85.4%	Score	3383.2;
Matches	3555;	Pred. No.	0;
Conservative	0;	Mismatches	3;
		Indels	130;
		Gaps	3;
Qy	277	AGAGATGCTGCCACCCCTAGGCCAGGGATCAGGCTATGGACAGAGGCC	336
Db	2	AGAGATGCTGCCACCCCTAGGCCAGGGATCAGGCTATGGACAGAGGCC	61
Qy	337	TGTCATCTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	396
Db	62	TGTCATCTTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	121
Qy	397	TGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	456
Db	122	TGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	181
Qy	457	ACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	516
Db	182	ACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	241
Qy	517	GGATGACGGGGATGGGCGCTGTGCTGCTGCTGCTGCTGCTG	576
Db	242	GGATGACGGGGATGGGCGCTGTGCTGCTGCTGCTGCTGCTG	301
Qy	577	ACTTGAGGTGATCTACCTCCACTGTGCTGCTGCTGCTGCTG	636
Db	302	ACTTGAGGTGATCTACCTCCACTGTGCTGCTGCTGCTGCTG	361
Qy	637	ATGCCGGGGCTGGGAGGAGTCTCCGGAGTACCGGTGCTGGAT	696
Db	362	ATGCCGGGGCTGGGAGGAGTCTCCGGAGTACCGGTGCTGGAT	421
Qy	697	GTGCCCTGGGGCTGGGAGGAGCCTGGGTAGGAGGTGATCTG	756

Qy	2917	TCTTCGGGACAGGGCGGAGGTGTACCTGTCGCCGCTGCCTGCCAGGGC	2976	RESULT	12
Db	2513	TCTTCGGGACAGGGCGGAGGTGTACCTGTCGCCGCTGCCTGCCAGGGC	2572	HSPKE	
Qy	2977	TATATGAGCTGATCTTCGGTGTGGCTGGAGCTGAGAGACGACACCTT	3036	LOCUS	HSTRKE
Db	2573	TATATGAGCTGATCTTCGGTGTGGCTGGAGCTGAGAGACGACACCTT	2632	DEFINITION	H.sapiens TRK E mRNA.
Qy	3037	AGCTGCATGGTCTGGCAGAGATGACTACAGGTGTAATCACITCCAGCT	3096	VERSION	X74919.1 GI:400462
Db	2633	AGCTGCATGGTCTGGCAGAGATGACTACAGGTGTAATCACITCCAGCT	2692	KEYWORDS	trk E gene; Trk E protein.
Qy	3097	CCCTCCCTCAGGGAGTATCCAGGGACGTGACTAACAGAGGACATG	3156	SOURCE	human.
Db	2693	CCCTCCCTCAGGGAGTATCCAGGGACGTGACTAACAGAGGACATG	2752	ORGANISM	Homo sapiens
Qy	3157	GACCTCTGCCCTCCCTCCACAGCCATCACCTTAATAGAGGAGTGA	3216	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Db	2753	GACACTCTGCCCTCCCTCCACAGCCATCACCTTAATAGAGGAGTGA	2692	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Qy	3217	GTTGGGCTGGGCCACCCAGGAGCTGATGCCCTTCCCTTGAGACACT	3276	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
Db	2813	GTTGGGCTGGGCCACCCAGGAGCTGATGCCCTTCCCTTGAGACACT	2872	REFERENCE	1. (bases 1 to 3554)
Qy	3277	TGCCCCATCCCTCTCTCTAGAGCCCTGCGCCACCCAGCTGCCCTG	3336	Di Marco, E., Cuttilli, N., Guerra, L., Canevella, R. and De Luca, M.	
Db	2873	TGCCCCATCCCTCTCTAGAGCCCTGCGCCACCCAGCTGCCCTG	2932	AUTHORS	Molecular cloning of trkE, a novel trk-related putative tyrosine
Qy	3337	ATGGATCTCTCCACCCCTCTAGCATCCCTGGGAAGGGAGATA	3396	TITLE	'kinase receptor isolated from normal human keratinocytes and widely
Db	2933	ATGGATCTCTCCACCCCTCTAGCATCCCTGGGAAGGGAGATA	2992	expressed by normal human tissues	
Qy	3397	ATAGACACTGGCATGGCCCATGGACCTGGCCCCACTGGACACAT	3456	JOURNAL	J. Biol. Chem. 268 (32), 24290-24295 (1993)
Db	2993	ATAGACACTGGCATGGCCCATGGACCTGGACACATGATCCG	3052	MEDLINE	9404265
Qy	3457	GAGAGGGCTGCTGGCCAGGCTCTGGCACACTGGACCCACTGGCTG	3515	2. (bases 1 to 3554)	
Db	3053	GAGAGGGCTGCTGCCGCCAGCTCTCTCTGTCACACTGGACCCACTGGCTG	3112	De Luca, M.	
Qy	3516	GAACTCTGGGGCTGGAGGACAGAAGAGGAGAAATGTTCTTGCTGCT	3575	FEATURES	TITLE
Db	3113	GAACTCTGGGGCTGGAGGACAGAAGAGGAGAAATGTTCTTGCTGCT	3172	gene	Direct Submission
Qy	3576	ACTGTCTCTGAGGAGGACAGACACTGGACCTGGCTGGGAGTA	3635	gene	Submitted (08-SEP-1993) M. De Luca, Istituto Nazionale Per la
Db	3173	ACTGTCTCTGAGGAGGACAGACACTGGACCTGGCTGGGAGTA	3232	cds	Ricerca sul Cancro, Lab Differenziazione Cellulare, Viale Benedetto XV, 10 - 16132 Genova, ITALY
Qy	3636	GGCCGGCCACACCTCTGGCACCCACTTGCACTGGCTGGAGTAA	3695	source	Location/Qualifiers
Db	3233	GGCCGGCCACACCTCTGGCACCCACTTGCACTGGCTGGAGTAA	3292	1. 3554	1. /organism="Homo sapiens"
Qy	3696	TCTAAGCTATGGTCTGGAGTAATATGGCATGGGAGGAGGACAA	3755	/translation="MPEAALSLLILVLSAGDADMKHDPAKCRYALGMQDRTPD	
Db	3293	TCTAAGCTATGGTCTGGAGTAATATGGCATGGGAGGAGGACAA	3352	SDISASSWDSTAAHRSLLESSDGAGCPAGSPYFPEKQFVYDQDRLHLVLYGT	
Qy	3756	GGCCATAGCTGCTGGGGAGGACATCTAGTGCACTGGAGTAA	3815	QGRHAGLGKEFSEYRLRSRDRGWRMGKDRMQEYVSGNEPEGVYVLDQPMV	
Db	3353	GGCCATAGCTGCTGGGGAGGACATCTAGTGCACTGGAGTAA	3412	ARLVEYPRADRVMSVCLRLVYGLWDRDLSVYIAPVGQTMJSEAVLNDSTYDGH	
Qy	3816	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	TIVGQYGGQGLADQVGLDFRISQELRVEWVMSHESSEAFDR	
Db	3413	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	TKNAROMVQCNMHTGALPUGVECERPGPAMWEPRMNPRLNGDPRARV	
Qy	3876	TGCTTGAGGCAATTATTAATGCCCTGACTTGCACTGGAGTAA	3935	SVPLGGRVFLQCHFLKAGFWLSEISISDVNNSSALGGFPKAWPPGPPP	
Db	3473	TGCTTGAGGCAATTATTAATGCCCTGACTTGCACTGGAGTAA	3532	TNFSSLERPRQQVKAAGSPWTLVLLCILVLLTALMLWHRMLRLLA	
Qy	3936	ACGAGCTGCTGCCACCCCTAGGCCAGGGTCAGGCTATGGCCAGAGCC	3532	ERRVLEELVWVSPGDTLINRPGPRPPRPPRPPRPPRPPRPPRPPRPPR	
Db	3533	ACGAGCTGCTGCCACCCCTAGGCCAGGGTCAGGCTATGGCCAGAGCC	3412	DMEERKGPPLPQNSVPHADTIVLQYQGIGNTYAVKPLPAGVGDPPR	
Qy	3817	GGCCATAGCTGCTGGGGAGGACATCTAGTGCACTGGAGTAA	3875	DFPRRLRFFKLGPGQFQGVHCEVDSODLPLVNRKPLVAVLKLPD	
Db	3414	GGCCATAGCTGCTGGGGAGGACATCTAGTGCACTGGAGTAA	3472	TKNAROMVQCNMHTGALPUGVECERPGPAMWEPRMNPRLNGDPRARV	
Qy	3937	TGCTTGAGGCAATTATTAATGCCCTGACTTGCACTGGAGTAA	3532	DKAEGAGDQGQANQGPTISYPMUHLVQAGQASGRKLATLNFHDLRMLRMLV	
Db	3534	TGCTTGAGGCAATTATTAATGCCCTGACTTGCACTGGAGTAA	3412	FTIKLADFGMSRNLLAGDYLVRQGAVLPWMECTLNGKFTWASQF	
Qy	3938	GGCCATAGCTGCTGGGGAGGACATCTAGTGCACTGGAGTAA	3532	VLMICRAQPGOLDEOYENAGERFRDQGRQVLSRPPACPPQGQYLMRCHWSRE	
Db	3535	GGCCATAGCTGCTGGGGAGGACATCTAGTGCACTGGAGTAA	3412	ORPPESQHFLDAFLNLY"	
Qy	3818	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	BASE COUNT	682
Db	3415	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	a 1064	
Qy	3819	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	c 1065	
Db	3416	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3820	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	g 9	
Db	3417	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3821	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	a 9	
Db	3418	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	c 743	
Qy	3822	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3419	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	g 743	
Qy	3823	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3420	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	a 743	
Qy	3824	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	c 9	
Db	3421	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3825	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	g 9	
Db	3422	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3826	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	a 9	
Db	3423	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	c 743	
Qy	3827	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3424	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	g 743	
Qy	3828	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3425	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	a 743	
Qy	3829	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	c 9	
Db	3426	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3830	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	g 9	
Db	3427	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3831	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	a 9	
Db	3428	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	c 743	
Qy	3832	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3429	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	g 743	
Qy	3833	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3430	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	a 743	
Qy	3834	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	c 9	
Db	3431	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3835	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	g 9	
Db	3432	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3836	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	a 9	
Db	3433	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	c 743	
Qy	3837	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3434	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	g 743	
Qy	3838	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3435	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	a 743	
Qy	3839	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	c 9	
Db	3436	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3840	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	g 9	
Db	3437	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3841	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	a 9	
Db	3438	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	c 743	
Qy	3842	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3439	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	g 743	
Qy	3843	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3440	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	a 743	
Qy	3844	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	c 9	
Db	3441	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3845	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	g 9	
Db	3442	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3846	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	a 9	
Db	3443	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	c 743	
Qy	3847	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3444	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	g 743	
Qy	3848	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	t 9	
Db	3445	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	a 743	
Qy	3849	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	c 9	
Db	3446	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3472	t 743	
Qy	3850	ACTGGGGTTGCTACATTTGGGGAGAGACAGATTTACATTAATGGAC	3875	g 9	

Db	122	TGATCTGCAAGTGCCTATGCCCTGGCATGCAGACCGACATCCAGACAGTG	Db	1202	GGCCGCTGGCCACCTCCACCAACTTCAGCAGCTTGAGCTTGAGGCCAGAGGCCAGC	1261
Qy	457	ACATCTCTCTTCAGCTCTGGTCAGATTCACGCCCGCACAGCAGGTTGACA	Qy	1537	AGCCGTTGCCAAAGGCCAGGGAGGGAGCCACCCCATCTCGGCTGCCCTGGCCA	1596
Db	182	ACATCTCTCTTCAGCTCTGGTCAGATTCACGCCCGCACAGCAGGTTGACA	Db	1262	AGCCGTTGCCAAAGGCCAGGGAGGGAGCCACCCCATCTCGGCTGCCCTGGCCA	1321
Qy	517	GCAGTGACGGGAGGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG	Qy	1597	TCATCTCTCTGTCATCATTCGGCTCATGCTCTGGGCTGCACTGGGCTGCC	1656
Db	242	GCAGTGACGGGAGGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG	Db	1322	TCATCTCTCTGTCATCATTCGGCTCATGCTCTGGGCTGCACTGGGCTGCC	1381
Qy	577	ACTTGCAAGTGTGAACTACACGACTCCACCTGGGAGCTGTTGGGACCCAGGAGC	Qy	1657	TCCTAGCAGGCTGAAAGGGGTTGAAAGGAGGAGGAGGAGGAGGAGGAGGAG	1716
Db	302	ACTTGCAAGTGTGAACTACACGACTCCACCTGGGAGCTGTTGGGACCCAGGAGC	Db	1382	TCCTAGCAGGCTGAAAGGGGTTGAAAGGAGGAGGAGGAGGAGGAGGAGGAG	1441
Qy	637	ATGCCGGGGCTGGCAAGGAAGTCTCCCGGACCTACCGGCTGGCTGAGGAGGAG	Qy	1717	CTGGGACACTATCTCATCACACACCCACGGCTGGCTGAGGAGGAGGAGGAG	1776
Db	362	ATGCCGGGGCTGGCAAGGAAGTCTCCCGGACCTACCGGCTGGCTGAGGAGGAG	Db	1442	CTGGGACACTATCTCATCACACCCACGGCTGGCTGAGGAGGAGGAGGAG	1501
Qy	697	GTGCCGCGCTGGTGGCTGGCTGGCTGGGAGGACCCCTGGGCTGAGGAGGAG	Qy	1777	AGCCCGACCTGGGATCCGGCCCATGTTGGCTGAGGAGGAGGAGGAGGAG	1836
Db	422	GTGCCGCGCTGGTGGCTGGCTGGCTGGCTGGCTGAGGAGGAGGAGGAGGAG	Db	1502	AGCCCGACCTGGGATCCGGCCCATGTTGGCTGAGGAGGAGGAGGAGGAG	1557
Qy	757	ACCTGTAGGGAGTGTGCTGGCAAGGACTGGGCCCCATGGTGGCTGAGGAGGAG	Qy	1837	TGCTGCTTCCATCACACCTACGCCCTCTGGGACTTACGCCCTACGCCCTGGAG	1896
Db	482	ACCTGTAGGGAGTGTGCTGGGCCCCATGGTGGCTGAGGAGGAGGAGGAGGAG	Db	1558	-----	1557
Qy	817	TCTACCCCGGCTGACCGGGCATGAGTGTGCTGGGCTGAGGAGGAGGAGGAG	Qy	1897	GCCGGGCCCCACACCCGCTGGGCAAAACCAACACCCACGGCTACAGTGGGG	1956
Db	542	TCTACCCCGGCTGACCGGGCATGAGTGTGCTGGGCCCCATGGGAGGAGGAGGAG	Db	1558	-----	-----
Qy	877	TCTGTAGGGATGACTCTGCTACCGCCCTGTGGAGACAACTGTATTTATCTG	Qy	1957	ACTATATGAGCTGAGGAGCCGGCCACCCGACCCAGGAGGAGGAGGAGGAG	2016
Db	662	AGCCGCTGTACCTCACTGACTCACCTATGAGGACATACCGGGGGACTGAGT	Db	1631	TCCCCATATGCGGAGGCTGACATTTACCTGCGGCCCCACCTCCCGAGACAG	1690
Qy	997	GGGCTCTGGCAAGTGTGCTGGAGTGGTGGGGCTGTGATGACTTAAAGAAGTAGG	Qy	2017	TCCCATATGCGGAGGCTGACATTTACCTGCGGCCCCACGGGGCAACACT	2076
Db	782	GGGCTCTGGCAAGTGTGCTGGGGCTGTGATGACTTAAAGAAGTAGG	Db	1691	ATGCTGCTGCTGACTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1750
Qy	1117	GCTATGTGGAGTGGACTTGTGTTGACCGCTGAGCACCACAGCTCTCCAGT	Qy	2137	CTGATCTGACTCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2196
Db	842	GCTATGTGGAGTGGACTTGTGTTGACCGCTGAGGAGCTCCAGCTGAGT	Db	1751	CTGATCTGACTCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1810
Qy	1177	ACTGTAACACATGCAACACGGCTGGAGGCCCTGCTGTGGGGTGAATGTCGCT	Qy	2257	AGGACACCTTGTGCTGGAGCTCAGATTTACGGCAGATGTCACAGTGTGCT	2136
Db	902	ACTGTAACACATGCAACACGGCTGGAGGCCCTGCTGTGGGGTGAATGTCGCT	Db	1871	AGGACACCTTGTGCTGGAGCTCAGATTTACGGCAGATGTCACAGTGTGCT	2256
Qy	1297	TGGGGACCCCTGGAGGCCGGCTGTGCTGGAGGCCCTGCTGTGGGGTGAATGTCGCT	Qy	2317	CTGCTCTCTGTCTGGAGGATGTTCTGAAAGGAGGAGGAGGAGGAGGAGG	2376
Db	1022	TGGGGACCCCTGGAGGCCGGCTGTGCTGGAGGCCCTGCTGTGGGGTGAATGTCGCT	Db	1928	-----	-----
Qy	1357	TGCACTGGCTCTCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAG	Qy	2437	TTACTGACTATGGAGACGCGGAGCTCAACAGITTCCTGAGGAGGAGGAGGAG	2496
Db	1082	TGCACTGGCTCTCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAGGCCCTGGAG	Db	2033	TTACTGACTATGGAGACGCGGAGCTCAACAGITTCCTGAGGAGGAGGAGGAG	2092
Qy	1417	CTGATGTGGAGACAATTCTCTCTGGGAGCCACTGGGAGGAGGAGGAGGAGGAG	Qy	2497	ACAGGGAGGAGGGGGCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2556
Db	1142	CTGATGTGGAGACAATTCTCTCTGGGAGCCACTGGGAGGAGGAGGAGGAGGAG	Db	2093	ACAGGGAGGAGGGGGCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2152
Qy	1477	GGCCGAGCTGCACTCCACCAACTTCAGGAGCTGGAGGCCAGAGGCCAGC	Qy	2557	ACCAATGCTGCTGCTGGCAGGCCAGATGCGCTCCGCGCATGCGCTACTAGCCAC	2616
Db	2153	ACCAATGCTGCTGCTGGCAGGCCAGATGCGCTCCGCGCATGCGCTACTAGCCAC	Db	2153	ACCAATGCTGCTGCTGGCAGGCCAGATGCGCTCCGCGCATGCGCTACTAGCCAC	2212

QY	2617	TCACTTGTACATGGGACCTGGCCACGGGACTGCTTACTGGGAAATTACCA	2676
Db	2213	TCACTTGTACATGGGACCTGGCCACGGGACTGCTTACTGGGAAATTACCA	2272
QY	2677	TCAAATGGAGACTTGGCATAGGGAACTCTATGGGGACTATACCGTGC	2736
Db	2273	TCAAATGGAGACTTGGCATAGGGAACTCTATGGGGACTATACCGTGC	2332
QY	2737	AGGGCCGGAGCTGGCTCCCATCGCGTGGATGCGCTGGAGCATCTATGGGAA	2796
Db	2333	AGGGCCGGAGCTGGCTCCCATCGCGTGGATGCGCTGGAGCATCTATGGGAA	2392
QY	2857	GTAGGGCCACGCCCTGGGACCTAACGGAGAGGAGGATCTGAGAACGGGGAGT	2916
Db	2453	GTAGGGCCACGCCCTGGGACCTAACGGAGAGGAGGATCTGAGAACGGGGAGT	2512
QY	2917	TCTTCCGGGACGCCCTGGGACAGGTCACCTGAGGAGGATCTGAGAACGGGGC	2976
Db	2513	TCTTCCGGGACGCCCTGGGACAGGTCACCTGAGGAGGATCTGAGAACGGGGC	2572
QY	2977	TATATGAGCTGATGCTGGCTGGAGCCGGAGCTGAGGAGGATCTGAGAACGGGC	3036
Db	2573	TATATGAGCTGATGCTGGCTGGAGCCGGAGCTGAGGAGGATCTGAGAACGGGC	2632
QY	3037	AGCTGCATCGGCTCTGGAGGATCTAACACGGTGAACTACACCTCAGCTG	3096
Db	2633	AGCTGCATCGGCTCTGGAGGATCTAACACGGTGAACTACACCTCAGCTG	2692
QY	3097	CCCTCTCTAGGGAGGTGATCCAGGGAGGAGCAGTGACATTAACAGAGGACATG	3156
Db	2693	CCCTCTCTAGGGAGGTGATCCAGGGAGGAGCAGTGACATTAACAGAGGACATG	2752
QY	3157	GCACCTCTGGCCCTCCCTCCGACAGGCCCATCACCTATAGAGGAGCTGCA	3216
Db	2753	GCACCTCTGGCCCTCCCTCCGACAGGCCCATCACCTATAGAGGAGCTGCA	2812
QY	3217	GTGGGCTGGGCCACCCAGGAGCAGTGACCTGGGAAAGCCAGACTCTCA	3276
Db	2813	GTGGGCTGGGCCACCCAGGAGCAGTGACCTGGGAAAGCCAGACTCTCA	2872
QY	3277	TGTCCCTTCT	3336
Db	2873	TGTCCCTTCT	2932
QY	3337	ATGGGATCCCTCACCCCTCTAGGCATCTGGGGAGGGAGAATATAGG	3396
Db	2933	ATGGGATCCCTCACCCCTCTAGGCATCTGGGGAGGGAGAATATAGG	2992
QY	3397	ATAGACACTGGCATGCCATGGGACCTGGGCCCACTGGACACACTGATCTG	3456
Db	2993	ATAGACACTGGCATGCCATGGGACCTGGGCCCACTGGACACACTGATCTG	3052
QY	3457	GAGAGCTGGCTGCGG-CGCCACTTCCTCTCTCTCTCTCTCTCTCTCTCT	3515
Db	3053	GAGAGCTGGCTGCGGCCCACTTCCTCTCTCTCTCTCTCTCTCTCTCTCT	3112
QY	3516	GAATCTGGGGTGGAGGAGGAGGAAATGTTCTGTGGCTCTGT	3575
Db	3113	GAATCTGGGGTGGAGGAGGAGGAAATGTTCTGTGGCTCTGT	3172
QY	3576	ACTTGCTGCTCAGCTGGGCTCTCCCTCCATACCTAACACTGGACCTGSGGTA	3635
Db	3173	ACTTGCTGCTCAGCTGGGCTCTCCCTCCATACCTAACACTGGACCTGSGGTA	3232
QY	3636	GCCCCGCCAGCCCTGAGCACCCCACTTCCACTTGGACTCTGACTAGACTC	3695
Db	3233	GCCCCGCCAGCCCTGAGCACCCCACTTCCACTTGGACTCTGACTAGACTC	3292
QY	3696	TCTAGGCCTATACCTTCTGTGGAGTAANTTGGATGGGGAGGGAGGACACG	3755
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AUTHORS	1 (bases 1 to 3841); Laval,S., Butler,R., Shelling,A.N., Hanby,A.M., Pouliom,R. and Ganeshan,T.S.		
REFERENCE	2 (bases 1 to 3841); Shelling,A.N., Butler,R., Jones,T., Laval,S., Boyle,J.M. and Ganeshan,T.S.		
AUTHORS	Isolation and characterization of an epithelial-specific receptor tyrosine kinase from an ovarian cancer cell line		
TITLE	JOURNAL		
	Cell Growth Differ.		
JOURNAL	5 (11), 1173-1183 (1994)		
MEDLINE	95151638		
REFERENCE	3 (bases 1 to 3841); Kedinger,C.		
AUTHORS	Direct Submission		
TITLE	JOURNAL		
	Genomics		
JOURNAL	25 (2), 584-587 (1995)		
MEDLINE	9530932		
REFERENCE	3 (bases 1 to 3841); Kedinger,C.		
AUTHORS	Localization of an epithelial-specific receptor kinase (EDDR1) to chromosome 6q16		
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Db	2984	CCCTCCCTGAGGAGGACATCCAGGGAGGCGCTGACACTAACAGAGACACATG	3043	AUTHORS	Perez, J.L., Jing, S.Q. and Wong, T.W.		
			TITLE	Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines			

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Db	662	CCCCATGGTGGCCAGCTGCTGCTACCCCGGTCACCGCTCATGAGCT 721			
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